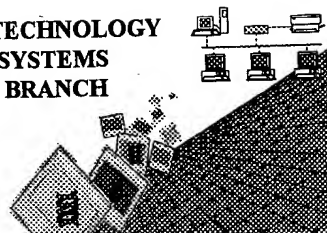


BIOTECHNOLOGY
SYSTEMS
BRANCH



0570
0423

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/821,782A
Source: OIPB
Date Processed by STIC: 4/24/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

01PE

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/821,782A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>
Sequence(s) 215 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



**Does Not Comply
Corrected Diskette Needed**

OIKE

RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/09/821,782A

TIME: 14:09:40

Input Set : A:\821782seq.txt

Output Set: N:\CRF3\04242002\I821782A.raw

4 <110> APPLICANT: Kumar Verma, Sunil
 5 Singh, Lalji
 7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION
 9 <130> FILE REFERENCE: U-013365-9
 11 <140> CURRENT APPLICATION NUMBER: 09/821782A
 C--> 13 <141> CURRENT FILING DATE: 2002-04-08
 15 <160> NUMBER OF SEQ ID NOS: 255

ERRORED SEQUENCES

4304 <210> SEQ ID NO: 215
 4306 <211> LENGTH: 22
 4308 <212> TYPE: DNA
 4310 <213> ORGANISM: Artificial Sequence
 W--> 4312 <220> FEATURE: *Missing <220> Feature - required, see item 11 on error summary sheet*
 4312 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b
 4313 gene of animal species in polymerase chain reaction
 ok E--> 4315 <400> SEQUENCE: 215
 4318 atgcaaatag gaagtatcat tc 22
 4916 <210> SEQ ID NO: 244
 4918 <211> LENGTH: 472
 4920 <212> TYPE: DNA
 4922 <213> ORGANISM: Ovis vignei *error, see p. 3 for explanation (item 9 on error summary sheet)*
 4924 <400> SEQUENCE: 244
 4926 taccatgagg acaaatatca ttctgaggag caacagttat taccaacctc ctttcagcaa 60
 4927 ttccatatat tggcaciaaac ctatctgaat gaatctgagg aggattctca gtagacaaag 120
 4928 ctaccctcac ccgatttttc gcctttcact ttattttccc attcatcatc gcagccctcg 180
 4929 ctatagttca cctactcttc ctccacgaaa caggatccaa taaccccaca ggaattccat 240
 E--> 4930 cggacacaga caaaatcccc ttccccnnnnnn nnnnnnnnat taaagacatt ctgggtgcca 300
 4931 tctactaat cctcatcctc atgctgctag tactattcac gcctgactta cttggagacc 360
 4932 cagacaacta caccacgca aaccactta aactcccc tcacatcaaa cctgaatgat 420
 4933 atttcctatt tgcatatgca atcttacgat caatccctaa taaactagga gg 472
 5112 <210> SEQ ID NO: 254
 5114 <211> LENGTH: 472
 5116 <212> TYPE: DNA
 5118 <213> ORGANISM: Cervus elaphus xanthopygus
 5120 <400> SEQUENCE: 254
 5122 taccatgagg acaaatatca ttctgaggag caacgggtcat taccaacctt ctctcagcaa 60
 5123 ttccatacat tggcaciaaac ctatctgaat ggatctgagg aggcttttca gtagataaag 120
 5124 caaccetaac ccgatttttc gctttccact ttattctccc atttatcatc gcagcactcg 180
 5125 ctatagtaca cttactcttc cttcacgaga caggatccaa taacccaaca ggaattccat 240
 5126 cagacgcaga caaaatcccc ttccatcctt actataccat taaagatatc ttaggcattc 300

RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/09/821,782A

TIME: 14:09:41

Input Set : A:\821782seq.txt

Output Set: N:\CRF3\04242002\I821782A.raw

5127	tacttctagt	actcttccta	atattactag	tattattcgc	accagacctg	cttggagacc	360
5128	cagacaacta	taccccagca	aatccactca	acacaccccc	tcacattaaa	cctgaatgat	420
5129	atttcctatt	tgcatacgca	atcctacgat	cgattcccaa	caaactagga	gg	472

E--> 5132 ① -delete (non-ascii garbage)

VARIABLE LOCATION SUMMARY

DATE: 04/24/2002

PATENT APPLICATION: US/09/821,782A

TIME: 14:09:42

Input Set : A:\821782seq.txt

Output Set: N:\CRF3\04242002\I821782A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:45; N Pos. 269,431

Seq#:216; N Pos. 104,107,128,368,369,431

Seq#:217; N Pos. 425,431

Seq#:226; N Pos. 437

Seq#:240; N Pos. 264,338

Seq#:244; N Pos. 264,265,266,267,268,269,270,271,272,273,274,275,276,277

Seq#:244; N Pos. 278

VERIFICATION SUMMARY

DATE: 04/24/2002

PATENT APPLICATION: US/09/821,782A

TIME: 14:09:42

Input Set : A:\821782seq.txt

Output Set: N:\CRF3\04242002\I821782A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:967 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:240
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:420
L:4312 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:215
L:4315 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:215
L:4331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:216
L:4340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:60
L:4341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:120
L:4345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:360
L:4346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216 after pos.:420
L:4358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:217
L:4373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217 after pos.:420
L:4546 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:226
L:4561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:226 after pos.:420
L:4829 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:240
L:4842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:240
L:4843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:300
L:4909 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:243
L:4930 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:244
L:5132 M:254 E: No. of Bases conflict, this line has no nucleotides.